

SEQUENCE LISTING

<110> Fraunhofer Gesellschaft zur Förderung der angewandten Forschung
e.V.

<120> Immunokinases

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<140> PCT/EP2005/050131

<141> 2005-01-13

<150> 04000847.6

<151> 2004-01-16

<150> 04017928.5

<151> 2004-07-29

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<170> PatentIn Ver. 2.1

<210> 1

<211> 1785

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:

pMS-(L-DAPK2'-Ki-4)-III/G open reading frame (ORF)

<220>

<221> CDS

<222> (1)..(1785)

<220>

<221> N_region

<222> (1)..(21)

<223> immunoglobulin kappa chain leader sequence

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ggt tcc act ggt gac tct aga atg gtc cag gcc tcg atg agg agc cca
Gly Ser Thr Gly Asp Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro
20 25 30

aat atg gag acg ttc aaa cag cag aag gtg gag gac ttt tat gat att
Asn Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile
35 40 45

gga gag gag ctg ggc agt ggc cag ttt gcc atc gtg aag aag tgc cgg
Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg
50 55 60

gag aag agc acg ggg ctg gag tat gca gcc aag ttc att aag aag agg Glu Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg 65 70 75 80	240
cag agc cgg gcc agc cgt cgg ggc gtg tgc cgg gag gaa atc gag cgg Gln Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg 85 90 95	288
gag gtg agc atc ctg cgg cag gtg ctg cac ccc aac atc atc acg ctg Glu Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu 100 105 110	336
cac gac gtc tat gag aac cgc acc gac gtg gtg ctc atc ctt gag cta His Asp Val Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu 115 120 125	384
gtg tcc gga gga gaa ctg ttt gat ttc ctg gcc cag aag gag tcg tta Val Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu 130 135 140	432
agt gag gag gaa gcc acc agc ttc att aag cag atc ctg gat ggg gtg Ser Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val 145 150 155 160	480
aat tac ctt cac aca aag aaa att gct cac ttt gat ctc aag cca gaa Asn Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu 165 170 175	528
aac atc atg ttg tta gac aag aat atc cca att cca cac atc aag ctg Asn Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu 180 185 190	576
att gac ttt ggc ctg gct cac gaa ata gaa gat gga gtt gaa ttt aaa Ile Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys 195 200 205	624
aac att ttt ggg aca cct gaa ttt gtt gct cca gaa atc gtg aac tat Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr 210 215 220	672
gag cca ctg gga ctg gag gcc gac atg tgg agc att gga gtc atc acc Glu Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr 225 230 235 240	720
tat atc ctt cta agt gga gcg tcc ccc ttc ctg gga gac aca aaa caa Tyr Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln 245 250 255	768
gaa acc ctg gca aat atc act gct gtg agt tac gac ttt gat gag gaa Glu Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu 260 265 270	816
ttc ttc agc cag aca agc gag ctg gcc aag gac ttc att cgg aag ctt Phe Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu 275 280 285	864

ctt gtg aaa gag acc cgg aaa cgg ctt acc atc caa gag gct ctc aga Leu Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg 290	295	300	912	
cat ccc tgg atc gga tcc aaa cta gct gag cac gaa ggt gac gcg gcc His Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Gly Asp Ala Ala 305	310	315	320	960
cag ccg gcc atg gcc cag gtc aag ctg cag gag tca ggg act gaa ctg Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr Glu Leu 325	330	335	1008	
gca aag cct ggg gcc gca gtg aag atg tcc tgc aag gct tct ggc tac Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser Gly Tyr 340	345	350	1056	
acc ttt act gac tac tgg atg cac tgg gtt aaa cag agg cct gga cag Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln 355	360	365	1104	
ggt ctg gaa tgg att gga tac att aat cct aac act gct tat act gac Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr Thr Asp 370	375	380	1152	
tac aat cag aaa ttc aag gac aag gcc aca ttg act gca gac aaa tcc Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser 385	390	395	400	1200
tcc agc aca gcc tac atg caa ctg cgc agc ctg acc tct gag gat tct Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu Asp Ser 405	410	415	1248	
gca gtc tat tac tgt gca aaa aag aca act cag act acg tgg ggg ttt Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp Gly Phe 420	425	430	1296	
cct ttt tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt gga ggc Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly 435	440	445	1344	
ggt tca ggc gga ggt ggc tct ggc ggt ggc gga tcg gac att gtg ctg Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser Asp Ile Val Leu 450	455	460	1392	
acc cag tct cca aaa tcc atg gcc atg tca gtc gga gag agg gtc acc Thr Gln Ser Pro Lys Ser Met Ala Met Ser Val Gly Glu Arg Val Thr 465	470	475	480	1440
ttg agc tgc aag gcc agt gag aat gtg gat tct ttt gtt tcc tgg tat Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser Trp Tyr 485	490	495	1488	
caa cag aaa cca ggc cag tct cct aaa ctg ctg ata tac ggg gcc tcc Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser 500	505	510	1536	

aac	cggtacactgggttc	cccgatcgcttc	gca	ggc	agt	gga	tct	gga	1584							
Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Ala	Gly	Ser	Gly	Ser	Gly	
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aga	gatttcactctgacc	atc	agc	agt	gtgtc	cag	gct	gaa	gac	ctt	gca	1632				
Arg	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala	
530					535					540						
gat	tatcac	tgt	gga	cag	aat	tac	agg	tat	ccg	ctc	acg	ttc	ggt	gct	1680	
Asp	Tyr	His	Cys	Gly	Gln	Asn	Tyr	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Ala	
545					550					555					560	
ggc	acc	aag	ctg	gaa	atc	aaa	cg	gcg	gcc	gca	ggg	ccc	gaa	caa	aaa	1728
Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ala	Ala	Gly	Pro	Glu	Gln	Lys		
565					570					575						
ctc	atc	tca	gaa	gag	gat	ctg	aat	agc	gcc	gtc	gac	cat	cat	cat	cat	1776
Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Ser	Ala	Val	Asp	His	His	His	His	
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His	His															
595																

<210> 2

<211> 594

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence:

pMS-(L-DAPK2'-Ki-4)-III/G open reading frame (ORF)

<400> 2

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Gly	Ser	Thr	Gly	Asp	Ser	Arg	Met	Val	Gln	Ala	Ser	Met	Arg	Ser	Pro
							20		25				30		
Asn	Met	Glu	Thr	Phe	Lys	Gln	Gln	Lys	Val	Glu	Asp	Phe	Tyr	Asp	Ile
							35		40			45			
Gly	Glu	Glu	Leu	Gly	Ser	Gly	Gln	Phe	Ala	Ile	Val	Lys	Lys	Cys	Arg
							50		55			60			
Glu	Lys	Ser	Thr	Gly	Leu	Glu	Tyr	Ala	Ala	Lys	Phe	Ile	Lys	Lys	Arg
							65		70			75			80
Gln	Ser	Arg	Ala	Ser	Arg	Arg	Gly	Val	Cys	Arg	Glu	Ile	Glu	Arg	
							85		90			95			
Glu	Val	Ser	Ile	Leu	Arg	Gln	Val	Leu	His	Pro	Asn	Ile	Ile	Thr	Leu
							100		105			110			
His	Asp	Val	Tyr	Glu	Asn	Arg	Thr	Asp	Val	Val	Leu	Ile	Leu	Glu	Leu
							115		120			125			
Val	Ser	Gly	Gly	Glu	Leu	Phe	Asp	Phe	Leu	Ala	Gln	Lys	Glu	Ser	Leu
							130		135			140			
Ser	Glu	Glu	Glu	Ala	Thr	Ser	Phe	Ile	Lys	Gln	Ile	Leu	Asp	Gly	Val
							145		150			155			160
Asn	Tyr	Leu	His	Thr	Lys	Lys	Ile	Ala	His	Phe	Asp	Leu	Lys	Pro	Glu
							165		170			175			
Asn	Ile	Met	Leu	Leu	Asp	Lys	Asn	Ile	Pro	Ile	Pro	His	Ile	Lys	Leu

180	185	190
Ile Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val	Glu Phe Lys	
195	200	205
Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr		
210	215	220
Glu Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr		
225	230	235
Tyr Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln		240
245	250	255
Glu Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu		
260	265	270
Phe Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu		
275	280	285
Leu Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg		
290	295	300
His Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Gly Asp Ala Ala		
305	310	315
Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr Glu Leu		320
325	330	335
Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser Gly Tyr		
340	345	350
Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln		
355	360	365
Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr Thr Asp		
370	375	380
Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser		
385	390	395
Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu Asp Ser		400
405	410	415
Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp Gly Phe		
420	425	430
Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly		
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450	455	460
Thr Gln Ser Pro Lys Ser Met Ala Met Ser Val Gly Glu Arg Val Thr		
465	470	475
Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser Trp Tyr		480
485	490	495
Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser		
500	505	510
Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ala Gly Ser Gly Ser Gly		
515	520	525
Arg Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala		
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Asp Tyr His Cys Gly Gln Asn Tyr Arg Tyr Pro Leu Thr Phe Gly Ala		
545	550	555
Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Gly Pro Glu Gln Lys		560
565	570	575
Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His		
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His His		

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<211> 1794
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:
      pMS-(Ki-4-DAPK2')-II/G ORF

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<222> (1)..(1794)

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<222> (1)..(21)
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1           5           10          15

ggc tcc act ggt gac gcg gcc cag ccg gcc atg gcc cag gtc aag ctg      96
Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu
20          25          30

cag gag tca ggg act gaa ctg gca aag cct ggg gcc gca gtg aag atg      144
Gln Glu Ser Gly Thr Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met
35          40          45

tcc tgc aag gct tct ggc tac acc ttt act gac tac tgg atg cac tgg      192
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp
50          55          60

gtt aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att aat      240
Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
65          70          75          80

cct aac act gct tat act gac tac aat cag aaa ttc aag gac aag gcc      288
Pro Asn Thr Ala Tyr Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala
85          90          95

aca ttg act gca gac aaa tcc tcc agc aca gcc tac atg caa ctg cgc      336
Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg
100         105         110

agc ctg acc tct gag gat tct gca gtc tat tac tgt gca aaa aag aca      384
Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr
115         120         125

act cag act acg tgg ggg ttt cct ttt tgg ggc caa ggg acc acg gtc      432
Thr Gln Thr Thr Trp Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val
130         135         140

acc gtc tcc tca ggt gga ggc ggt tca ggc gga ggt ggc tct ggc ggt      480
Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly

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145	150	155	160	
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tca gtc gga gag agg gtc acc ttg agc tgc aag gcc agt gag aat gtg Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val 180	185		190	576
gat tct ttt gtt tcc tgg tat caa cag aaa cca ggc cag tct cct aaa Asp Ser Phe Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 195	200		205	624
ctg ctg ata tac ggg gcc tcc aac cgg tac act ggg gtc ccc gat cgc Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg 210	215	220		672
ttc gca ggc agt gga tct gga aga gat ttc act ctg acc atc agc agt Phe Ala Gly Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser 225	230	235	240	720
gtg cag gct gaa gac ctt gca gat tat cac tgt gga cag aat tac agg Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg 245	250		255	768
tat ccg ctc acg ttc ggt gct ggc acc aag ctg gaa atc aaa cgg gcg Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala 260	265	270		816
gcc gca ctc gag tct aga atg gtc cag gcc tcg atg agg agc cca aat Ala Ala Leu Glu Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro Asn 275	280	285		864
atg gag acg ttc aaa cag cag aag gtg gag gac ttt tat gat att gga Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile Gly 290	295	300		912
gag gag ctg ggc agt ggc cag ttt gcc atc gtg aag aag tgc cgg gag Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg Glu 305	310	315	320	960
aag agc acg ggg ctg gag tat gca gcc aag ttc att aag aag agg cag Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Arg Gln 325	330	335		1008
agc cgg gcc agc cgt cgg ggc gtg tgc cgg gag gaa atc gag cgg gag Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg Glu 340	345	350		1056
gtg agc atc ctg cgg cag gtg ctg cac ccc aac atc atc acg ctg cac Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu His 355	360	365		1104
gac ctc tat gag aac cgc acc gac gtg gtg ctc atc ctt gag cta gtg Asp Leu Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu Val				1152

370	375	380	
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gag gag gaa gcc acc agc ttc att aag cag atc ctg gat ggg gtg aat Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val Asn 405 410 415			1248
tac ctt cac aca aag aaa att gct cac ttt gat ctc aag cca gaa aac Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu Asn 420 425 430			1296
atc atg ttg tta gac aag aat atc cca att cca cac atc aag ctg att Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu Ile 435 440 445			1344
gac ttt ggc ctg gct cac gaa ata gaa gat gga gtt gaa ttt aaa aac Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys Asn 450 455 460			1392
att ttt ggg aca cct gaa ttt gtt gct cca gaa atc gtg aac tat gag Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu 465 470 475 480			1440
cca ctg gga ctg gag gcc gac atg tgg agc att gga gtc atc acc tat Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr 485 490 495			1488
atc ctt cta agt gga gcg tcc ccc ttc ctg gga gac aca aaa caa gaa Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu 500 505 510			1536
acc ctg gca aat atc act gct gtg agt tac gac ttt gat gag gaa ttc Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu Phe 515 520 525			1584
ttc agc cag aca agc gag ctg gcc aag gac ttc att cgg aag ctt ctt Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu Leu 530 535 540			1632
gtg aaa gag acc cg ^g aaa cg ^g ctt acc atc caa gag gct ctc aga cat Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg His 545 550 555 560			1680
ccc tgg atc gga tcc aaa cta gct gag cac gaa ttt cga gga ggg ccc Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Phe Arg Gly Gly Pro 565 570 575			1728
gaa caa aaa ctc atc tca gaa gag gat ctg aat agc gcc gtc gac cat Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His 580 585 590			1776
cat cat cat cat cat tga His His His His His			1794

595

<210> 4
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<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:
pMS-(Ki-4-DAPK2')-II/G ORF

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35 40 45
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp
50 55 60
Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
65 70 75 80
Pro Asn Thr Ala Tyr Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala
85 90 95
Thr Leu Thr Ala Asp Lys Ser Ser Thr Ala Tyr Met Gln Leu Arg
100 105 110
Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr
115 120 125
Thr Gln Thr Thr Trp Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val
130 135 140
Thr Val Ser Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly 160
145 150 155
Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met
165 170 175
Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val
180 185 190
Asp Ser Phe Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
195 200 205
Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
210 215 220
Phe Ala Gly Ser Gly Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser
225 230 235 240
Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg
245 250 255
Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala
260 265 270
Ala Ala Leu Glu Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro Asn
275 280 285
Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile Gly
290 295 300
Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg Glu
305 310 315 320
Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Gln
325 330 335
Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg Glu
340 345 350
Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu His

355	360	365
Asp Leu Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu Val		
370	375	380
Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu Ser		
385	390	395
Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val Asn		
405	410	415
Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu Asn		
420	425	430
Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu Ile		
435	440	445
Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys Asn		
450	455	460
Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu		
465	470	475
Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr		
485	490	495
Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu		
500	505	510
Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu Phe		
515	520	525
Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu Leu		
530	535	540
Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg His		
545	550	555
Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Phe Arg Gly Gly Pro		
565	570	575
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His		
580	585	590
His His His His		
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: pMT-Ki-4
(scFv) -eEF-2K ORF

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gcc cag ccg gcg atg gcc atg ggc cat cat cat cat cat cat cat cat cat	96
Ala Gln Pro Ala Met Ala Met Gly His His His His His His His His	
20 25 30	
cat cac agc agc ggc cat atc gac gac gac aag cat atg aag ctt	144
His His Ser Ser Gly His Ile Asp Asp Asp Lys His Met Lys Leu	
35 40 45	
atg gcc cag ccg gcc atg gcc cag gtc aag ctg cag gag tca ggg act	192
Met Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr	
50 55 60	
gaa ctg gca aag cct ggg gcc gca gtg aag atg tcc tgc aag gct tct	240
Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser	
65 70 75 80	
ggc tac acc ttt act gac tac tgg atg cac tgg gtt aaa cag agg cct	288
Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro	
85 90 95	
gga cag ggt ctg gaa tgg att gga tac att aat cct aac act gct tat	336
Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr	
100 105 110	
act gac tac aat cag aaa ttc aag gac aag gcc aca ttg act gca gac	384
Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp	
115 120 125	
aaa tcc tcc agc aca gcc tac atg caa ctg cgc agc ctg acc tct gag	432
Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu	
130 135 140	
gat tct gca gtc tat tac tgt gca aaa aag aca act cag act acg tgg	480
Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp	
145 150 155 160	
ggg ttt cct ttt tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt	528
Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly	
165 170 175	
gga ggc ggt tca ggc gga ggt ggc tct ggc ggt ggc gga tcg gac att	576
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile	
180 185 190	
gtg ctg acc cag tct cca aaa tcc atg gcc atg tca gtc gga gag agg	624
Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met Ser Val Gly Glu Arg	
195 200 205	
gtc acc ttg agc tgc aag gcc agt gag aat gtg gat tct ttt gtt tcc	672
Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser	
210 215 220	
tgg tat caa cag aaa cca ggc cag tct cct aaa ctg ctg ata tac ggg	720
Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Gly	
225 230 235 240	

gcc tcc aac cgg tac act ggg gtc ccc gat cgc ttc gca ggc agt gga Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ala Gly Ser Gly 245 250 255	768
tct gga aga gat ttc act ctg acc atc agc agt gtg cag gct gaa gac Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp 260 265 270	816
ctt gca gat tat cac tgt gga cag aat tac agg tat ccg ctc acg ttc Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg Tyr Pro Leu Thr Phe 275 280 285	864
ggg gct ggc acc aag ctg gaa atc aaa cgg gcg gcc gca gag ctc ggc Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu Leu Gly 290 295 300	912
gga ggt ggc tct atg gca gac gaa gat ctc atc ttc cgc ctg gaa ggc Gly Gly Ser Met Ala Asp Glu Asp Leu Ile Phe Arg Leu Glu Gly 305 310 315 320	960
gtt gat ggc ggc cag tcc ccc cga gct ggc cat gat ggt gat tct gat Val Asp Gly Gly Gln Ser Pro Arg Ala Gly His Asp Gly Asp Ser Asp 325 330 335	1008
ggg gac agc gac gat gag gaa ggt tac ttc atc tgc ccc atc acg gat Gly Asp Ser Asp Asp Glu Glu Gly Tyr Phe Ile Cys Pro Ile Thr Asp 340 345 350	1056
gac cca agc tcg aac cag aat gtc aat tcc aag gtt aat aag tac tac Asp Pro Ser Ser Asn Gln Asn Ser Lys Val Asn Lys Tyr Tyr 355 360 365	1104
agc aac cta aca aaa agt gag cgg tat agc tcc agc ggg tcc ccc gca Ser Asn Leu Thr Lys Ser Glu Arg Tyr Ser Ser Gly Ser Pro Ala 370 375 380	1152
aac tcc ttc cac ttc aag gaa gcc tgg aag cac gca atc cag aag gcc Asn Ser Phe His Phe Lys Glu Ala Trp Lys His Ala Ile Gln Lys Ala 385 390 395 400	1200
aag cac atg ccc gac ccc tgg gct gag ttc cac ctg gaa gat att gcc Lys His Met Pro Asp Pro Trp Ala Glu Phe His Leu Glu Asp Ile Ala 405 410 415	1248
acc gaa cgt gct act cga cac agg tac aac gcc gtc acc ggg gaa tgg Thr Glu Arg Ala Thr Arg His Arg Tyr Asn Ala Val Thr Gly Glu Trp 420 425 430	1296
ctg gat gat gaa gtt ctg atc aag atg gca tct cag ccc ttc ggc cga Leu Asp Asp Glu Val Leu Ile Lys Met Ala Ser Gln Pro Phe Gly Arg 435 440 445	1344
gga gca atg agg gag tgc ttc cgg acg aag ctc tcc aac ttc ttg Gly Ala Met Arg Glu Cys Phe Arg Thr Lys Lys Leu Ser Asn Phe Leu 450 455 460	1392

cat gcc cag cag tgg aag ggc gcc tcc aac tac gtg gcg aag cgc tac His Ala Gln Gln Trp Lys Gly Ala Ser Asn Tyr Val Ala Lys Arg Tyr 465 470 475 480 485 490 495 1440	1440
atc gag ccc gta gac cggtt gat gtg tac ttt gag gac gtg cgt cta cag Ile Glu Pro Val Asp Arg Asp Val Tyr Phe Glu Asp Val Arg Leu Gln 485 490 495 1488	1488
atg gag gcc aag ctc tgg ggg gag gag tat aat cgg cac aag ccc ccc Met Glu Ala Lys Leu Trp Gly Glu Tyr Asn Arg His Lys Pro Pro 500 505 510 1536	1536
aag cag gtg gac atc atg cag atg tgc atc atc gag ctg aag gac aga Lys Gln Val Asp Ile Met Gln Met Cys Ile Ile Glu Leu Lys Asp Arg 515 520 525 1584	1584
ccg ggc aag ccc ctc ttc cac ctg gag cac tac atc gag ggc aag tac Pro Gly Lys Pro Leu Phe His Leu Glu His Tyr Ile Glu Gly Lys Tyr 530 535 540 1632	1632
atc aag tac aac tcc aac tct ggc ttt gtc cgc gat gac aac atc cgc Ile Lys Tyr Asn Ser Asn Ser Gly Phe Val Arg Asp Asp Asn Ile Arg 545 550 555 560 1680	1680
ctg acg ccg cag gcc ttc agc cac ttc act ttt gag cgt tcc ggc cat Leu Thr Pro Gln Ala Phe Ser His Phe Thr Phe Glu Arg Ser Gly His 565 570 575 1728	1728
cag ctg ata gtg gtg gac atc cag gga gtt ggg gat ctc tac act gac Gln Leu Ile Val Val Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp 580 585 590 1776	1776
cca cag atc cac acg gag acg ggc act gac ttt gga gac ggc aac cta Pro Gln Ile His Thr Glu Thr Gly Thr Asp Phe Gly Asp Gly Asn Leu 595 600 605 1824	1824
ggg gtc cgc ggg atg ggc ctc ttc tac tct cat gcc tgc aac cgg Gly Val Arg Gly Met Ala Leu Phe Phe Tyr Ser His Ala Cys Asn Arg 610 615 620 1872	1872
att tgc gag agc atg ggc ctt gct ccc ttt gac ctc tcg ccc cgg gag Ile Cys Glu Ser Met Gly Leu Ala Pro Phe Asp Leu Ser Pro Arg Glu 625 630 635 640 1920	1920
agg gat gca gtg aat cag aac acc aag ctg ctg caa tca gcc aag acc Arg Asp Ala Val Asn Gln Asn Thr Lys Leu Leu Gln Ser Ala Lys Thr 645 650 655 1968	1968
atc ttg aga gga aca gag gaa aaa tgt ggg agc ccc cga gta agg acc Ile Leu Arg Gly Thr Glu Glu Lys Cys Gly Ser Pro Arg Val Arg Thr 660 665 670 2016	2016
ctc tct ggg agc cgg cca ccc ctg ctc cgt ccc ctt tca gag aac tct Leu Ser Gly Ser Arg Pro Pro Leu Leu Arg Pro Leu Ser Glu Asn Ser 675 680 685 2064	2064

gga gac gag aac atg agc gac gtg acc ttc gac tct ctc cct tct tcc Gly Asp Glu Asn Met Ser Asp Val Thr Phe Asp Ser Leu Pro Ser Ser 690 695 700	2112
cca tct tcg gcc aca cca cac agc cag aag cta gac cac ctc cat tgg Pro Ser Ser Ala Thr Pro His Ser Gln Lys Leu Asp His Leu His Trp 705 710 715 720	2160
cca gtc ttc agt gac ctc gat aac atg gca tcc aga gac cat gat cat Pro Val Phe Ser Asp Leu Asp Asn Met Ala Ser Arg Asp His Asp His 725 730 735	2208
cta gac aac cac cg ^g gag tct gag aat agt ggg gac agc gga tac ccc Leu Asp Asn His Arg Glu Ser Glu Asn Ser Gly Asp Ser Gly Tyr Pro 740 745 750	2256
agt gag aag cg ^g ggt gag ctg gat gac cct gag ccc cga gaa cat ggc Ser Glu Lys Arg Gly Glu Leu Asp Asp Pro Glu Pro Arg Glu His Gly 755 760 765	2304
cac tca tac agt aat cg ^g aag tac gag tct gac gaa gac agc ctg ggc His Ser Tyr Ser Asn Arg Lys Tyr Glu Ser Asp Glu Asp Ser Leu Gly 770 775 780	2352
agc tct gga cg ^g gta tgt gta gag aag tgg aat ctc ctc aac tcc tcc Ser Ser Gly Arg Val Cys Val Glu Lys Trp Asn Leu Leu Asn Ser Ser 785 790 795 800	2400
cgc ctc cac ctg cg ^g agg gct tcg gcc gtg gcc ctg gaa gtg caa agg Arg Leu His Leu Pro Arg Ala Ser Ala Val Ala Leu Glu Val Gln Arg 805 810 815	2448
ctt aat gct ctg gac ctc gaa aag aaa atc ggg aag tcc att ttg ggg Leu Asn Ala Leu Asp Leu Glu Lys Lys Ile Gly Lys Ser Ile Leu Gly 820 825 830	2496
aag gtc cat ctg gcc atg gtg cgc tac cac gag ggt ggg cgc ttc tgc Lys Val His Leu Ala Met Val Arg Tyr His Glu Gly Arg Phe Cys 835 840 845	2544
gag aag gg ^g gag gag tgg gac gag tcg gct gtc ttc cac ctg gag Glu Lys Gly Glu Glu Trp Asp Gln Glu Ser Ala Val Phe His Leu Glu 850 855 860	2592
cac gca gcc aac ctg gg ^g gag ctg gag gcc atc gtg ggc ctg gga ctc His Ala Ala Asn Leu Gly Glu Leu Glu Ala Ile Val Gly Leu Gly Leu 865 870 875 880	2640
atg tac tcg cag ttg cct cat cac atc cta gcc gat gtc tct ctg aag Met Tyr Ser Gln Leu Pro His His Ile Leu Ala Asp Val Ser Leu Lys 885 890 895	2688
gag aca gaa gag aac aaa acc aaa gga ttt gat tac tta cta aag gcc Glu Thr Glu Glu Asn Lys Thr Lys Gly Phe Asp Tyr Leu Leu Lys Ala 900 905 910	2736

gct gaa gct ggc gac agg cag tcc atg atc cta gtg gcg cga gct ttt Ala Glu Ala Gly Asp Arg Gln Ser Met Ile Leu Val Ala Arg Ala Phe 915 920 925	2784
gac tct ggc cag aac ctc agc ccg gac agg tgc caa gac tgg cta gag Asp Ser Gly Gln Asn Leu Ser Pro Asp Arg Cys Gln Asp Trp Leu Glu 930 935 940	2832
gcc ctg cac tgg tac aac act gcc ctg gag atg acg gac tgt gat gag Ala Leu His Trp Tyr Asn Thr Ala Leu Glu Met Thr Asp Cys Asp Glu 945 950 955 960	2880
ggc ggt gag tac gac gga atg cag gag ccc cgg tac atg atg ctg Gly Gly Glu Tyr Asp Gly Met Gln Asp Glu Pro Arg Tyr Met Met Leu 965 970 975	2928
gcc agg gag gcc gag atg ctg ttc aca gga ggc tac ggg ctg gag aag Ala Arg Glu Ala Glu Met Leu Phe Thr Gly Gly Tyr Gly Leu Glu Lys 980 985 990	2976
gac ccg cag aga tca ggg gac ttg tat acc cag gca gca gag gca gcg Asp Pro Gln Arg Ser Gly Asp Leu Tyr Thr Gln Ala Ala Glu Ala Ala 995 1000 1005	3024
atg gaa gcc atg aag ggc cga ctg gcc aac cag tac tac caa aag gct Met Glu Ala Met Lys Gly Arg Leu Ala Asn Gln Tyr Tyr Gln Lys Ala 1010 1015 1020	3072
gaa gag gcc tgg gcc cag atg gag gag taa Glu Glu Ala Trp Ala Gln Met Glu Glu 1025 1030	3102

<210> 6
<211> 1033
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: pMT-Ki-4
(scFv) -eEF-2K ORF

<400> 6
Met Lys Tyr Leu Leu Pro Thr Ala Ala Gly Leu Leu Leu Ala
1 5 10 15
Ala Gln Pro Ala Met Ala Met Gly His His His His His His
20 25 30
His His Ser Ser Gly His Ile Asp Asp Asp Asp Lys His Met Lys Leu
35 40 45
Met Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr
50 55 60
Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser
65 70 75 80
Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro
85 90 95
Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr
100 105 110

Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp
115 120 125
Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu
130 135 140
Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp
145 150 155 160
Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
165 170 175
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile
180 185 190
Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met Ser Val Gly Glu Arg
195 200 205
Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser
210 215 220
Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Gly
225 230 235 240
Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ala Gly Ser Gly
245 250 255
Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp
260 265 270
Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg Tyr Pro Leu Thr Phe
275 280 285
Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu Leu Gly
290 295 300
Gly Gly Gly Ser Met Ala Asp Glu Asp Leu Ile Phe Arg Leu Glu Gly
305 310 315 320
Val Asp Gly Gly Gln Ser Pro Arg Ala Gly His Asp Gly Asp Ser Asp
325 330 335
Gly Asp Ser Asp Asp Glu Glu Gly Tyr Phe Ile Cys Pro Ile Thr Asp
340 345 350
Asp Pro Ser Ser Asn Gln Asn Val Asn Ser Lys Val Asn Lys Tyr Tyr
355 360 365
Ser Asn Leu Thr Lys Ser Glu Arg Tyr Ser Ser Ser Gly Ser Pro Ala
370 375 380
Asn Ser Phe His Phe Lys Glu Ala Trp Lys His Ala Ile Gln Lys Ala
385 390 395 400
Lys His Met Pro Asp Pro Trp Ala Glu Phe His Leu Glu Asp Ile Ala
405 410 415
Thr Glu Arg Ala Thr Arg His Arg Tyr Asn Ala Val Thr Gly Glu Trp
420 425 430
Leu Asp Asp Glu Val Leu Ile Lys Met Ala Ser Gln Pro Phe Gly Arg
435 440 445
Gly Ala Met Arg Glu Cys Phe Arg Thr Lys Lys Leu Ser Asn Phe Leu
450 455 460
His Ala Gln Gln Trp Lys Gly Ala Ser Asn Tyr Val Ala Lys Arg Tyr
465 470 475 480
Ile Glu Pro Val Asp Arg Asp Val Tyr Phe Glu Asp Val Arg Leu Gln
485 490 495
Met Glu Ala Lys Leu Trp Gly Glu Glu Tyr Asn Arg His Lys Pro Pro
500 505 510
Lys Gln Val Asp Ile Met Gln Met Cys Ile Ile Glu Leu Lys Asp Arg
515 520 525
Pro Gly Lys Pro Leu Phe His Leu Glu His Tyr Ile Glu Gly Lys Tyr
530 535 540
Ile Lys Tyr Asn Ser Asn Ser Gly Phe Val Arg Asp Asp Asn Ile Arg
545 550 555 560

Leu Thr Pro Gln Ala Phe Ser His Phe Thr Phe Glu Arg Ser Gly His
565 570 575
Gln Leu Ile Val Val Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp
580 585 590
Pro Gln Ile His Thr Glu Thr Gly Thr Asp Phe Gly Asp Gly Asn Leu
595 600 605
Gly Val Arg Gly Met Ala Leu Phe Phe Tyr Ser His Ala Cys Asn Arg
610 615 620
Ile Cys Glu Ser Met Gly Leu Ala Pro Phe Asp Leu Ser Pro Arg Glu
625 630 635 640
Arg Asp Ala Val Asn Gln Asn Thr Lys Leu Leu Gln Ser Ala Lys Thr
645 650 655
Ile Leu Arg Gly Thr Glu Glu Lys Cys Gly Ser Pro Arg Val Arg Thr
660 665 670
Leu Ser Gly Ser Arg Pro Pro Leu Leu Arg Pro Leu Ser Glu Asn Ser
675 680 685
Gly Asp Glu Asn Met Ser Asp Val Thr Phe Asp Ser Leu Pro Ser Ser
690 695 700
Pro Ser Ser Ala Thr Pro His Ser Gln Lys Leu Asp His Leu His Trp
705 710 715 720
Pro Val Phe Ser Asp Leu Asp Asn Met Ala Ser Arg Asp His Asp His
725 730 735
Leu Asp Asn His Arg Glu Ser Glu Asn Ser Gly Asp Ser Gly Tyr Pro
740 745 750
Ser Glu Lys Arg Gly Glu Leu Asp Asp Pro Glu Pro Arg Glu His Gly
755 760 765
His Ser Tyr Ser Asn Arg Lys Tyr Glu Ser Asp Glu Asp Ser Leu Gly
770 775 780
Ser Ser Gly Arg Val Cys Val Glu Lys Trp Asn Leu Leu Asn Ser Ser
785 790 795 800
Arg Leu His Leu Pro Arg Ala Ser Ala Val Ala Leu Glu Val Gln Arg
805 810 815
Leu Asn Ala Leu Asp Leu Glu Lys Lys Ile Gly Lys Ser Ile Leu Gly
820 825 830
Lys Val His Leu Ala Met Val Arg Tyr His Glu Gly Gly Arg Phe Cys
835 840 845
Glu Lys Gly Glu Glu Trp Asp Gln Glu Ser Ala Val Phe His Leu Glu
850 855 860
His Ala Ala Asn Leu Gly Glu Leu Glu Ala Ile Val Gly Leu Gly Leu
865 870 875 880
Met Tyr Ser Gln Leu Pro His His Ile Leu Ala Asp Val Ser Leu Lys
885 890 895
Glu Thr Glu Glu Asn Lys Thr Lys Gly Phe Asp Tyr Leu Leu Lys Ala
900 905 910
Ala Glu Ala Gly Asp Arg Gln Ser Met Ile Leu Val Ala Arg Ala Phe
915 920 925
Asp Ser Gly Gln Asn Leu Ser Pro Asp Arg Cys Gln Asp Trp Leu Glu
930 935 940
Ala Leu His Trp Tyr Asn Thr Ala Leu Glu Met Thr Asp Cys Asp Glu
945 950 955 960
Gly Gly Glu Tyr Asp Gly Met Gln Asp Glu Pro Arg Tyr Met Met Leu
965 970 975
Ala Arg Glu Ala Glu Met Leu Phe Thr Gly Gly Tyr Gly Leu Glu Lys
980 985 990
Asp Pro Gln Arg Ser Gly Asp Leu Tyr Thr Gln Ala Ala Glu Ala Ala
995 1000 1005

Met Glu Ala Met Lys Gly Arg Leu Ala Asn Gln Tyr Tyr Gln Lys Ala
1010 1015 1020
Glu Glu Ala Trp Ala Gln Met Glu Glu
1025 1030

<210> 7
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
linker

<400> 7
Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 8
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: c-Myc epitope

<400> 8
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 9
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: motif in
domain IX of kinases

<220>
<221> VARIANT
<222> (2)
<223> any amino acid

<220>
<221> VARIANT
<222> (4)..(5)
<223> any amino acid

<400> 9
Asp Xaa Trp Xaa Xaa Gly
1 5